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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/837,992

DATE: 10/11/2001

TIME: 09:29:54

Input Set : A:\-60-2.app

Output Set: N:\CRF3\10112001\I837992.raw

3 <110> APPLICANT: Tian, Hui
 4 Schultz, Joshua
 5 Shan, Bei
 6 Tularik Inc.
 8 <120> TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG): Compositions
 9 and Methods of Use
 11 <130> FILE REFERENCE: 018781-006020US
 13 <140> CURRENT APPLICATION NUMBER: US 09/837,992
 14 <141> CURRENT FILING DATE: 2001-04-18
 16 <150> PRIOR APPLICATION NUMBER: US 60/198,465
 17 <151> PRIOR FILING DATE: 2000-04-18
 19 <150> PRIOR APPLICATION NUMBER: US 60/204,234
 20 <151> PRIOR FILING DATE: 2000-05-15
 22 <160> NUMBER OF SEQ ID NOS: 45
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 652
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Mus musculus
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG)
 33 amino acid sequence
 35 <400> SEQUENCE: 1
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 37 1 5 10 15
 39 Ile Asn Arg Gly Ser Leu Ser Ser Leu Glu Gln Gly Ser Val Thr Gly
 40 20 25 30
 42 Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val
 43 35 40 45
 45 Ser Asn Arg Val Gly Pro Trp Trp Asn Ile Lys Ser Cys Gln Gln Lys
 46 50 55 60
 48 Trp Asp Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Ile Glu Ser Gly
 49 65 70 75 80
 51 Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu
 52 85 90 95
 54 Leu Asp Ala Ile Ser Gly Arg Leu Arg Arg Thr Gly Thr Leu Glu Gly
 55 100 105 110
 57 Glu Val Phe Val Asn Gly Cys Glu Leu Arg Arg Asp Gln Phe Gln Asp
 58 115 120 125
 60 Cys Phe Ser Tyr Val Leu Gln Ser Asp Val Phe Leu Ser Ser Leu Thr
 61 130 135 140
 63 Val Arg Glu Thr Leu Arg Tyr Thr Ala Met Leu Ala Leu Cys Arg Ser
 64 145 150 155 160
 66 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu
 67 165 170 175
 69 Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly
 70 180 185 190

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72 Gly Ile Ser Ser Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu
73 195 200 205
75 Leu Gln Asp Pro Lys Val Met Met Leu Asp Glu Pro Thr Thr Gly Leu
76 210 215 220
78 Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala
79 225 230 235 240
81 Arg Arg Asp Arg Ile Val Ile Val Thr Ile His Gln Pro Arg Ser Glu
82 245 250 255
84 Leu Phe Gln His Phe Asp Lys Ile Ala Ile Leu Thr Tyr Gly Glu Leu
85 260 265 270
87 Val Phe Cys Gly Thr Pro Glu Glu Met Leu Gly Phe Phe Asn Asn Cys
88 275 280 285
90 Gly Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp
91 290 295 300
93 Leu Thr Ser Val Asp Thr Gln Ser Arg Glu Arg Glu Ile Glu Thr Tyr
94 305 310 315 320
96 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr
97 325 330 335
99 His Lys Ile Leu Glu Asn Ile Glu Arg Ala Arg Tyr Leu Lys Thr Leu
100 340 345 350
102 Pro Met Val Pro Phe Lys Thr Lys Asp Pro Pro Gly Met Phe Gly Lys
103 355 360 365
105 Leu Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Met Arg Asn Lys
106 370 375 380
108 Gln Ala Val Ile Met Arg Leu Val Gln Asn Leu Ile Met Gly Leu Phe
109 385 390 395 400
111 Leu Ile Phe Tyr Leu Leu Arg Val Gln Asn Asn Thr Leu Lys Gly Ala
112 405 410 415
114 Val Gln Asp Arg Val Gly Leu Leu Tyr Gln Leu Val Gly Ala Thr Pro
115 420 425 430
117 Tyr Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Met Leu Arg Ala
118 435 440 445
120 Val Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr His Lys Trp Gln Met
121 450 455 460
123 Leu Leu Ala Tyr Val Leu His Val Leu Pro Phe Ser Val Ile Ala Thr
124 465 470 475 480
126 Val Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu Tyr Pro Glu
127 485 490 495
129 Val Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu
130 500 505 510
132 Ile Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro
133 515 520 525
135 Asn Ile Val Asn Ser Ile Val Ala Leu Leu Ser Ile Ser Gly Leu Leu
136 530 535 540
138 Ile Gly Ser Gly Phe Ile Arg Asn Ile Gln Glu Met Pro Ile Pro Leu
139 545 550 555 560
141 Lys Ile Leu Gly Tyr Phe Thr Phe Gln Lys Tyr Cys Cys Glu Ile Leu
142 565 570 575
144 Val Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Ser Asn

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145 580 585 590
147 Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln
148 595 600 605
150 Phe Ile Glu Lys Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Ala Asn
151 610 615 620
153 Phe Leu Ile Leu Tyr Gly Phe Ile Pro Ala Leu Val Ile Leu Gly Ile
154 625 630 635 640
156 Val Ile Phe Lys Val Arg Asp Tyr Leu Ile Ser Arg
157 645 650
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 2258
162 <212> TYPE: DNA
163 <213> ORGANISM: Mus musculus
165 <220> FEATURE:
166 <223> OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG)
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (47)..(2005)
171 <223> OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG)
172 protein
174 <400> SEQUENCE: 2
175 gggacaggcc actagaaaat tcacttgcatttgcttcctg ctagccatgg gtgagctgcc 60
176 ctttctgagt ccagagggag ccagaggccc tcacatcaac agagggtctc tgagctccct 120
177 ggagcaagggt tcggtcacgg gcacagaggc tcggcacagc ttaggtgtcc tgcattgtgc 180
178 ctacagcgctc agcaaccgtg tcgggccttg gtgaaacatc aaatcatgcc agcagaagtg 240
179 ggacaggcaa atcctcaaag atgtctcctt gtacatcgag agtggccaga ttatgtgcatt 300
180 ctttaggcagc tcaggctcag ggaagaccac gctgctggac gccatctccg ggaggctgcg 360
181 ggcgcactggg acccttggaaag gggaggttttgtaatggc tgcgagctgc gcagggacca 420
182 gttccaagac tgcttctcct acgtcctgca gagcagacgtt tttctgagca gcctcactgt 480
183 ggcgcagacg ttgcgataca cagcgatgtt ggcctctgc cgcagctccg cggacttcta 540
184 caacaagaag gtagaggcag tcatgacaga gctgagctg agccacgtgg cggaccaaatt 600
185 gattggcagc tataattttt gggaaatttc cagttggcag cggcgcggag tttccatcg 660
186 agcccaactc cttcaggacc ccaaggtcat gatgttagat gagccaacca caggactgga 720
187 ctgcatgact gcaaataaaa ttgtccttctt cttggctgag ctggctcgca gggaccgaat 780
188 tgtgattgtc accatccacc agcctcgctc tgagcttttc caacacttcg aaaaaattgc 840
189 catcctgact tacggagagt tgggtttctg tggcacccca gaggagatgc ttggcttctt 900
190 caataactgt gtttaccctt gtcctgaaca ttccaaatccc tttgattttt acatggactt 960
191 gacatcgatg gacacccaaa gcagagagcg ggaatataaa acgtacaagc ggtacagat 1020
192 gctggaatgt gccttcaagg aatctgacat ctatcacaaa attctggaga acattgaaag 1080
193 agcacgatac ctgaaaaccc tacccatgtt tccttcaaa aaaaaagatc ctcctggat 1140
194 gttcggcaag cttgggtgtcc tgctgaggcg agtaacaaga aacttaatga ggaataagca 1200
195 ggcagtgatt atgcgtctcg ttcagaatct gatcatggc ctcttcctca ttttcttacct 1260
196 tctccgcgtc cagaacaaca cgctaaaggg cgctgtgcag gaccgcgtgg ggctgctcta 1320
197 tcagcttgc ggtgcaccc catacaccgg catgctcaat gctgtgaatc tttttccat 1380
198 gctgagagcc gtcagcgacc aggagagtc ggtatggctg tatcataagt ggcagatgt 1440
199 gctgcctac gtgctacacg ttcctccctt cagcgtcatc gccacggta ttttcagcag 1500
200 tttgtttat tggactctgg gttgtatcc tgaagttgcc agatttgat atttctctgc 1560
201 tgctctttt gcccctcaact taattggaga atttctaaca cttgtgtgc ttggatatagt 1620
202 caaaaaccct aatattgtca acagtagatg ggctctgtc agcatctctg ggctgcttat 1680

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203 tggatctgga tttatcagaa acataacaaga aatgcccatt cctttaaaaa tcctgggtta 1740
 204 ttttacatc caaaaatact gttgtgagat tctcgtggtc aatgagttt acggcctgaa 1800
 205 cttcaactgt ggtggatcca acacctctat gctaaaatcac ccgatgtcg ccacaccca 1860
 206 aggggtccag ttcatcgaga aaacctgccc aggtgctaca tccagatca cggcaaactt 1920
 207 cctcatcttata tgggttta tcccagctct ggtcatccta ggaatagtga ttttaaagt 1980
 208 cagggactac ctgattagca gatagttaaatgacaggca ggaaagggtt aatgggcagg 2040
 209 caccccact gtggagcaca gagaagtact gtcttcaacc atcaggattt catctgcac 2100
 210 cttgtgtctt gacccttggt tctatccgga gccccaaaggcaac tcacagccct 2160
 211 ctgctattcc agcttgggg gcaatgtggt gcttggacat tgtactgaa ctggtccaaat 2220
 212 aatgtaaata ataataattc ataaacctac aggacatt 2258

215 <210> SEQ ID NO: 3
 216 <211> LENGTH: 651
 217 <212> TYPE: PRT
 218 <213> ORGANISM: Homo sapiens
 220 <220> FEATURE:
 221 <223> OTHER INFORMATION: human sitosterolemia susceptibility gene (SSG)
 222 amino acid sequence
 224 <400> SEQUENCE: 3

225 Met Gly Asp Leu Ser Ser Leu Thr Pro Gly Gly Ser Met Gly Leu Gln
 226 1 5 10 15
 228 Val Asn Arg Gly Ser Gln Ser Ser Leu Glu Gly Ala Pro Ala Thr Ala
 229 20 25 30
 231 Pro Glu Pro His Ser Leu Gly Ile Leu His Ala Ser Tyr Ser Val Ser
 232 35 40 45
 234 His Arg Val Arg Pro Trp Trp Asp Ile Thr Ser Cys Arg Gln Gln Trp
 235 50 55 60
 237 Thr Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Val Glu Ser Gly Gln
 238 65 70 75 80
 240 Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu Leu
 241 85 90 95
 243 Asp Ala Met Ser Gly Arg Leu Gly Arg Ala Gly Thr Phe Leu Gly Glu
 244 100 105 110
 246 Val Tyr Val Asn Gly Arg Ala Leu Arg Arg Glu Gln Phe Gln Asp Cys
 247 115 120 125
 249 Phe Ser Tyr Val Leu Gln Ser Asp Thr Leu Leu Ser Ser Leu Thr Val
 250 130 135 140
 252 Arg Glu Thr Leu His Tyr Thr Ala Leu Ala Ile Arg Arg Gly Asn
 253 145 150 155 160
 255 Pro Gly Ser Phe Gln Lys Lys Val Glu Ala Val Met Ala Glu Leu Ser
 256 165 170 175
 258 Leu Ser His Val Ala Asp Arg Leu Ile Gly Asn Tyr Ser Leu Gly Gly
 259 180 185 190
 261 Ile Ser Thr Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu Leu
 262 195 200 205
 264 Gln Asp Pro Lys Val Met Leu Phe Asp Glu Pro Thr Thr Gly Leu Asp
 265 210 215 220
 267 Cys Met Thr Ala Asn Gln Ile Val Val Leu Leu Val Glu Leu Ala Arg
 268 225 230 235 240
 270 Arg Asn Arg Ile Val Val Leu Thr Ile His Gln Pro Arg Ser Glu Leu

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271	245	250	255
273	Phe Gln Leu Phe Asp Lys Ile Ala Ile Leu Ser Phe Gly Glu Leu Ile		
274	260	265	270
276	Phe Cys Gly Thr Pro Ala Glu Met Leu Asp Phe Phe Asn Asp Cys Gly		
277	275	280	285
279	Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp Leu		
280	290	295	300
282	Thr Ser Val Asp Thr Gln Ser Lys Glu Arg Glu Ile Glu Thr Ser Lys		
283	305	310	315
285	Arg Val Gln Met Ile Glu Ser Ala Tyr Lys Lys Ser Ala Ile Cys His		
286	325	330	335
288	Lys Thr Leu Lys Asn Ile Glu Arg Met Lys His Leu Lys Thr Leu Pro		
289	340	345	350
291	Met Val Pro Phe Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu		
292	355	360	365
294	Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu		
295	370	375	380
297	Ala Val Ile Thr Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu		
298	385	390	395
300	Leu Phe Phe Val Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile		
301	405	410	415
303	Gln Asp Arg Val Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Pro Tyr		
304	420	425	430
306	Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val		
307	435	440	445
309	Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met		
310	450	455	460
312	Leu Ala Tyr Ala Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met		
313	465	470	475
315	Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val		
316	485	490	495
318	Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu Ile		
319	500	505	510
321	Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro Asn		
322	515	520	525
324	Ile Val Asn Ser Val Val Ala Leu Leu Ser Ile Ala Gly Val Leu Val		
325	530	535	540
327	Gly Ser Gly Phe Leu Arg Asn Ile Gln Glu Met Pro Ile Pro Phe Lys		
328	545	550	555
330	Ile Ile Ser Tyr Phe Thr Phe Gln Lys Tyr Cys Ser Glu Ile Leu Val		
331	565	570	575
333	Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Ser Ser Asn Val		
334	580	585	590
336	Ser Val Thr Thr Asn Pro Met Cys Ala Phe Thr Gln Gly Ile Gln Phe		
337	595	600	605
339	Ile Glu Lys Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Met Asn Phe		
340	610	615	620
342	Leu Ile Leu Tyr Ser Phe Ile Pro Ala Leu Val Ile Leu Gly Ile Val		
343	625	630	635
			640

VERIFICATION SUMMARY

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